

SEQUENCE LISTING

<110> Zlot, Constance H.  
Adema, Gosse J.  
Figdor, Carl  
Phillips, Joseph H.

<120> Mammalian Genes; Related Reagents and Methods

<130> DX1051Q

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<170> PatentIn Ver. 2.0

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<212> DNA  
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<222> (58)..(1467)

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Met Gly Ile Trp Thr Ser Gly Thr Asp Ile Phe Leu Ser Leu Trp Glu  
1 5 10 15

att tac gtg tct cca aga agc ccc gga tgg atg gac ttt atc cag cat 153  
Ile Tyr Val Ser Pro Arg Ser Pro Gly Trp Met Asp Phe Ile Gln His  
20 25 30

ttg gga gtt tgc tgt ttg gtt gct ctt att tca gtg ggc ctc ctg tct 201  
Leu Gly Val Cys Cys Leu Val Ala Leu Ile Ser Val Gly Leu Leu Ser  
35 40 45

gtg gcc gcc tgc tgg ttt ctg cca tca atc ata gcg gcc gct gcc tcc 249  
Val Ala Ala Cys Trp Phe Leu Pro Ser Ile Ile Ala Ala Ala Ser  
50 55 60

tgg att atc acg tgt gtt ctg ctg tgt tgc tcc aag cat gca cga tgt 297  
Trp Ile Ile Thr Cys Val Leu Leu Cys Cys Ser Lys His Ala Arg Cys  
65 70 75 80

ttt att ctt ctt gtc ttt ctc tct tgt ggc ctg cgt gaa ggc agg aat 345  
Phe Ile Leu Leu Val Phe Leu Ser Cys Gly Leu Arg Glu Gly Arg Asn  
85 90 95

gct ttg att gca gct ggc aca ggg atc gtc atc ttg gga cac gta gaa 393  
Ala Leu Ile Ala Ala Gly Thr Gly Ile Val Ile Leu Gly His Val Glu  
100 105 110

aat att ttt cac aac ttt aaa ggt ctc cta gat ggt atg act tgc aac Asn Ile Phe His Asn Phe Lys Gly Leu Leu Asp Gly Met Thr Cys Asn 115 120 125	441
cta agg gca aag agc ttt tcc ata cat ttt cca ctt ttg aaa aaa tat Leu Arg Ala Lys Ser Phe Ser Ile His Phe Pro Leu Leu Lys Lys Tyr 130 135 140	489
att gag gca att cag tgg att tat ggc ctt gcc act cca cta agt gta Ile Glu Ala Ile Gln Trp Ile Tyr Gly Leu Ala Thr Pro Leu Ser Val 145 150 155 160	537
ttt gat gac ctt gtt tct tgg aac cag acc ctg gca gtc tct ctt ttc Phe Asp Asp Leu Val Ser Trp Asn Gln Thr Leu Ala Val Ser Leu Phe 165 170 175	585
agt ccc agc cat gtc ctg gag gca cag cta aat gac agc aaa ggg gaa Ser Pro Ser His Val Leu Glu Ala Gln Leu Asn Asp Ser Lys Gly Glu 180 185 190	633
gtc ctg agc gtc ttg tac cag atg gca aca acc aca gag gtg ttg tcc Val Leu Ser Val Leu Tyr Gln Met Ala Thr Thr Glu Val Leu Ser 195 200 205	681
tcc ctg ggt cag aag cta ctt gcc ttt gca ggg ctt tcg ctc gtc ctg Ser Leu Gly Gln Lys Leu Leu Ala Phe Ala Gly Leu Ser Leu Val Leu 210 215 220	729
ctt ggc act ggc ctc ttc atg aag cga ttt ttg ggc cct tgt ggt tgg Leu Gly Thr Gly Leu Phe Met Lys Arg Phe Leu Gly Pro Cys Gly Trp 225 230 235 240	777
aag tat gaa aac atc tac atc acc aga caa ttt gtt cag ttt gat gaa Lys Tyr Glu Asn Ile Tyr Ile Thr Arg Gln Phe Val Gln Phe Asp Glu 245 250 255	825
agg gag aga cat caa cag agg ccc tgt gtg ctc ccg ctg aat aag gag Arg Glu Arg His Gln Gln Arg Pro Cys Val Leu Pro Leu Asn Lys Glu 260 265 270	873
gaa agg agg aag tat gtc atc atc ccg act ttc tgg ccg act cct aaa Glu Arg Arg Lys Tyr Val Ile Ile Pro Thr Phe Trp Pro Thr Pro Lys 275 280 285	921
gaa agg aaa aac ctg ggg ctg ttt ttc ctc ccc ata ctt atc cat ctc Glu Arg Lys Asn Leu Gly Leu Phe Phe Leu Pro Ile Leu Ile His Leu 290 295 300	969
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att ttc tca gtg agc aag cag ttt caa agc ttg cca ggg ttt gag gtt Ile Phe Ser Val Ser Lys Gln Phe Gln Ser Leu Pro Gly Phe Glu Val 325 330 335	1065

cac ttg aaa ctg cac gga gag aaa caa gga act caa gat att atc cat		1113	
His Leu Lys Leu His Gly Glu Lys Gln Gly Thr Gln Asp Ile Ile His			
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gat tct tcc ttt aat ata tct gtg ttt gaa ccc aac tgt atc cca aaa		1161	
Asp Ser Ser Phe Asn Ile Ser Val Phe Glu Pro Asn Cys Ile Pro Lys			
355	360	365	
cca aaa ttc ctt cta tct gag acc tgg gtt cct ctc agt gtt att ctt		1209	
Pro Lys Phe Leu Leu Ser Glu Thr Trp Val Pro Leu Ser Val Ile Leu			
370	375	380	
ttg ata tta gtg atg ctg gga ctg ttg tcc tct atc ctt atg caa ctt		1257	
Leu Ile Leu Val Met Leu Gly Leu Leu Ser Ser Ile Leu Met Gln Leu			
385	390	395	400
aaa atc ctg gtg tca gca tct ttc tac ccc agc gtg gag agg aag cgc		1305	
Lys Ile Leu Val Ser Ala Ser Phe Tyr Pro Ser Val Glu Arg Lys Arg			
405	410	415	
atc caa tat ctg cat gca aag ctg ctt aaa aaa aga tca aag cag ccg		1353	
Ile Gln Tyr Leu His Ala Lys Leu Leu Lys Lys Arg Ser Lys Gln Pro			
420	425	430	
ctg gga gaa gtc aaa aga cgg ctg agt ctc tat ctt aca aag att cat		1401	
Leu Gly Glu Val Lys Arg Arg Leu Ser Leu Tyr Leu Thr Lys Ile His			
435	440	445	
ttc tgg ctt cca gtc ctg aaa atg att agg aag aag caa atg gac atg		1449	
Phe Trp Leu Pro Val Leu Lys Met Ile Arg Lys Lys Gln Met Asp Met			
450	455	460	
gca agt gca gac aag tca tgagagaccc cgactactcc tcagccacat		1497	
Ala Ser Ala Asp Lys Ser			
465	470		
cgcaccaaca attctttca ggtctaggat ggcagtcaacttccatgataatagag		1557	
aactatgtga cgcagtcctc tcaggagtct gagttacag agccaaacttg cagcacctgg		1617	
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atctctacca cagcctcaca agcaaattgt aagggaaaca tacatgtaaa aagccagcaa		1857	
actatcttca aactcttccg tccttaatgt ctccatggc tattgccccca acaatggct		1917	
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Ile Tyr Val Ser Pro Arg Ser Pro Gly Trp Met Asp Phe Ile Gln His  
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Leu Gly Val Cys Cys Leu Val Ala Leu Ile Ser Val Gly Leu Leu Ser  
35 40 45

Val Ala Ala Cys Trp Phe Leu Pro Ser Ile Ile Ala Ala Ala Ser  
50 55 60

Trp Ile Ile Thr Cys Val Leu Leu Cys Cys Ser Lys His Ala Arg Cys  
65 70 75 80

Phe Ile Leu Leu Val Phe Leu Ser Cys Gly Leu Arg Glu Gly Arg Asn  
85 90 95

Ala Leu Ile Ala Ala Gly Thr Gly Ile Val Ile Leu Gly His Val Glu  
100 105 110

Asn Ile Phe His Asn Phe Lys Gly Leu Leu Asp Gly Met Thr Cys Asn  
115 120 125

Leu Arg Ala Lys Ser Phe Ser Ile His Phe Pro Leu Leu Lys Lys Tyr  
130 135 140

Ile Glu Ala Ile Gln Trp Ile Tyr Gly Leu Ala Thr Pro Leu Ser Val  
145 150 155 160

Phe Asp Asp Leu Val Ser Trp Asn Gln Thr Leu Ala Val Ser Leu Phe  
165 170 175

Ser Pro Ser His Val Leu Glu Ala Gln Leu Asn Asp Ser Lys Gly Glu  
180 185 190

Val Leu Ser Val Leu Tyr Gln Met Ala Thr Thr Glu Val Leu Ser  
195 200 205

Ser Leu Gly Gln Lys Leu Leu Ala Phe Ala Gly Leu Ser Leu Val Leu  
210 215 220

Leu Gly Thr Gly Leu Phe Met Lys Arg Phe Leu Gly Pro Cys Gly Trp  
225 230 235 240

Lys Tyr Glu Asn Ile Tyr Ile Thr Arg Gln Phe Val Gln Phe Asp Glu  
245 250 255

Arg Glu Arg His Gln Gln Arg Pro Cys Val Leu Pro Leu Asn Lys Glu  
260 265 270

Glu Arg Arg Lys Tyr Val Ile Ile Pro Thr Phe Trp Pro Thr Pro Lys  
275 280 285

Glu Arg Lys Asn Leu Gly Leu Phe Phe Leu Pro Ile Leu Ile His Leu

290

295

300

Cys Ile Trp Val Leu Phe Ala Ala Val Asp Tyr Leu Leu Tyr Arg Leu  
305 310 315 320

Ile Phe Ser Val Ser Lys Gln Phe Gln Ser Leu Pro Gly Phe Glu Val  
325 330 335

His Leu Lys Leu His Gly Glu Lys Gln Gly Thr Gln Asp Ile Ile His  
340 345 350

Asp Ser Ser Phe Asn Ile Ser Val Phe Glu Pro Asn Cys Ile Pro Lys  
355 360 365

Pro Lys Phe Leu Leu Ser Glu Thr Trp Val Pro Leu Ser Val Ile Leu  
370 375 380

Leu Ile Leu Val Met Leu Gly Leu Leu Ser Ser Ile Leu Met Gln Leu  
385 390 395 400

Lys Ile Leu Val Ser Ala Ser Phe Tyr Pro Ser Val Glu Arg Lys Arg  
405 410 415

Ile Gln Tyr Leu His Ala Lys Leu Leu Lys Lys Arg Ser Lys Gln Pro  
420 425 430

Leu Gly Glu Val Lys Arg Arg Leu Ser Leu Tyr Leu Thr Lys Ile His  
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Ala Ser Ala Asp Lys Ser  
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<223> Description of Artificial Sequence:reverse  
translation

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<221> misc\_feature

<222> (1)..(1410)

<223> n may be a, c, g, or t

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ytnathwsng tnggnytnty nwsngtngcn gcntgytggt tyytnccnws nathathgcn 180

gcnngcnw sntggathat hacntgygtn ytnyntgyt gywsnaarca ygcnmngntgy 240  
ttyathytny tngtnattytyt nwsntgyggn ytnmgngarg gnmgnaaygc nytnathgcn 300  
gcnngnacng gnathgtnat hytnggncay gtngaraaya httycayaa yttyaarggn 360  
ytnytngayg gnatgacntg yaayytnmgn gcnaarwsnt tywsnathca yttyccnytn 420  
ytnaaraart ayathgargc nathcartgg athtayggny tngcnacncc nytnwsngtn 480  
ttygaygayy tngtnwsntg gaaycaracn ytngcngtnw snytnattyws nccnwsncay 540  
gtnytngarg cncarytnaa ygaywsnaar ggngargtny tnwsngtnyt ntaycaratg 600  
gcnacnacna cngargtnyt nwsnwsnytn ggncaraary tnytngcnn ygcnggnytn 660  
wsnytngtny tnytnggnac nggnytnatty atgaarmgnt tyytnggncc ntgyggntgg 720  
aartaygara ayathtayat hacnmgnar ttygtncart tygaygarmg ngarmgnay 780  
carcarmgnc cntgygtnyt nccnytnaay aargargarm gnmgnarta ygtnathath 840  
ccnacnattyt ggccnacncc naargarmgn aaraayytn gnytnattytt yytnccnath 900  
ytnathcayy tntgyathtg ggtnytnatty gcnngcngtng aytayytnyt ntaymgnyn 960  
athttywsng tnwsnaarca rttycarwsn ytnccngnt tygargtnca yytnaarytn 1020  
cayggngara arcarggnac ncargayath athcaygayw snwsnttyaa yathwsngtn 1080  
ttygarccna aytgyathcc naarcnhaar tyyttnytnw sngaracntg ggtncnccnytn 1140  
wsngtnathy tnytnathyt ngtnatgytn ggnytnytnw snwsnathyt natgcarytn 1200  
aarathytn tnwsngcnws nttytayccn wsngtngarm gnaarmgnat hcartayytn 1260  
caygcnaary tnytnaaraa rmgnwsnaar carccnytn gngargtnaa rmgnmgnyn 1320  
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cac gcc gcc agg ccg gat tac aag gac gat gac aag atc gat ctg		96
His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Lys Ile Asp Leu		
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agc aaa tgc agg acc gtg gcg ggc ccc gtg ggg gga tcc ctg agt gtg		144
Ser Lys Cys Arg Thr Val Ala Gly Pro Val Gly Gly Ser Leu Ser Val		
15	20	25
cag tgt ccc tat gag aag gaa cac agg acc ctc aac aaa tac tgg tgc		192
Gln Cys Pro Tyr Glu Lys Glu His Arg Thr Leu Asn Lys Tyr Trp Cys		
30	35	40
aga cca cca cag att ttc cta tgt gac aag att gtg gag acc aaa ggg		240
Arg Pro Pro Gln Ile Phe Leu Cys Asp Lys Ile Val Glu Thr Lys Gly		
45	50	55
tca gca gga aaa agg aac ggc cga gtg tcc atc agg gac agt cct gca		288
Ser Ala Gly Lys Arg Asn Gly Arg Val Ser Ile Arg Asp Ser Pro Ala		
60	65	70 75
aac ctc agc ttc aca gtg acc ctg gag aat ctc aca gag gag gat gca		336
Asn Leu Ser Phe Thr Val Leu Glu Asn Leu Thr Glu Glu Asp Ala		
80	85	90
ggc acc tac tgg tgt ggg gtg gat aca ccg tgg ctc cga gac ttt cat		384
Gly Thr Tyr Trp Cys Gly Val Asp Thr Pro Trp Leu Arg Asp Phe His		
95	100	105
gat ccc gtt gtc gag gtt gag gtg tcc gtg ttc ccg gca tca acg tca		432
Asp Pro Val Val Glu Val Ser Val Phe Pro Ala Ser Thr Ser		
110	115	120
atg aca cct gca agt atc act gcg gcc aag acc tca aca atc aca act		480
Met Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr		
125	130	135
gca ttt cca cct gta tca tcc act acc ctg ttt gca gtg ggt gcc acc		528
Ala Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr		
140	145	150 155
cac agt gcc agc atc cag gag gaa act gag gag gtg gtg aac tca cag		576
His Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser Gln		
160	165	170
ctc ccg ctg ctc tcc ctg gca ttg ttg ctg ctt ctg ttg gtg		624
Leu Pro Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Leu Val		
175	180	185
ggg gcc tcc ctg cta gcc tgg agg atg ttt cag aaa tgg atc aaa gct		672
Gly Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala		
190	195	200
ggt gac cat tca gag ctg tcc cag aac ccc aag cag gct gcc acg cag		720

Gly	Asp	His	Ser	Glu	Leu	Ser	Gln	Asn	Pro	Lys	Gln	Ala	Ala	Thr	Gln	
205				210							215					
agt	gag	ctg	cac	tac	gca	aat	ctg	gag	ctg	ctg	atg	tgg	cct	ctg	cag	768
Ser	Glu	Leu	His	Tyr	Ala	Asn	Leu	Glu	Leu	Leu	Met	Trp	Pro	Leu	Gln	
220				225					230					235		
gaa	aag	cca	gca	cca	cca	agg	gag	gtg	gag	gtg	gaa	tac	agc	act	gtg	816
Glu	Lys	Pro	Ala	Pro	Pro	Arg	Glu	Val	Glu	Val	Glu	Tyr	Ser	Thr	Val	
240				245					250							
gcc	tcc	ccc	agg	gaa	gaa	ctt	cac	tat	gcc	tcg	gtg	gtg	ttt	gat	tct	864
Ala	Ser	Pro	Arg	Glu	Glu	Leu	His	Tyr	Ala	Ser	Val	Val	Phe	Asp	Ser	
255				260					265							
aac	acc	aac	agg	ata	gct	gct	cag	agg	cct	cg	gag	gag	gaa	cca	gat	912
Asn	Thr	Asn	Arg	Ile	Ala	Ala	Gln	Arg	Pro	Arg	Glu	Glu	Glu	Pro	Asp	
270				275					280							
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285				290												
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Ser	Lys	Cys	Arg	Thr	Val	Ala	Gly	Pro	Val	Gly	Gly	Ser	Leu	Ser	Val	
15				20								25				
Gln	Cys	Pro	Tyr	Glu	Lys	Glu	His	Arg	Thr	Leu	Asn	Lys	Tyr	Trp	Cys	
30				35							40					
Arg	Pro	Pro	Gln	Ile	Phe	Leu	Cys	Asp	Lys	Ile	Val	Glu	Thr	Lys	Gly	
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Ser	Ala	Gly	Lys	Arg	Asn	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Pro	Ala	
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Asn	Leu	Ser	Phe	Thr	Val	Thr	Leu	Glu	Asn	Leu	Thr	Glu	Glu	Asp	Ala	
80				85					90							
Gly	Thr	Tyr	Trp	Cys	Gly	Val	Asp	Thr	Pro	Trp	Leu	Arg	Asp	Phe	His	
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Asp	Pro	Val	Val	Glu	Val	Ser	Val	Phe	Pro	Ala	Ser	Thr	Ser			
110				115					120							

Met Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr  
125 130 135

Ala Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr  
140 145 150 155

His Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser Gln  
160 165 170

Leu Pro Leu Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Leu Val  
175 180 185

Gly Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala  
190 195 200

Gly Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln Ala Ala Thr Gln  
205 210 215

Ser Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met Trp Pro Leu Gln  
220 225 230 235

Glu Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu Tyr Ser Thr Val  
240 245 250

Ala Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val Val Phe Asp Ser  
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<222> (64)..(600)

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cac gcc gcc agg ccg gat tac aag gac gat gac gac aag atc gat atg 96  
His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Ile Asp Met  
-5 -1 1 5 10

aca cct gca agt atc act gcg aag acc tca aca atc aca act gca 144

Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr Ala			
15	20	25	
ttt cca cct gta tca tcc act acc ctg ttt gca gtg ggt gcc acc cac			192
Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr His			
30	35	40	
agt gcc agc atc cag gag gaa act gag gag gtg gtg aac tca cag ctc			240
Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser Gln Leu			
45	50	55	
ccg ctg ctc ctc tcc ctg gca ttg ttg ctg ctt ctg ttg gtg ggg			288
Pro Leu Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Leu Val Gly			
60	65	70	75
gcc tcc ctg cta gcc tgg agg atg ttt cag aaa tgg atc aaa gct ggt			336
Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala Gly			
80	85	90	
gac cat tca gag ctg tcc cag aac ccc aag cag gct gcc acg cag agt			384
Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln Ala Ala Thr Gln Ser			
95	100	105	
gag ctg cac tac gca aat ctg gag ctg ctg atg tgg cct ctg cag gaa			432
Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met Trp Pro Leu Gln Glu			
110	115	120	
aag cca gca cca cca agg gag gtg gag gtg gaa tac agc act gtg gcc			480
Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu Tyr Ser Thr Val Ala			
125	130	135	
tcc ccc agg gaa gaa ctt cac tat gcc tcg gtg gtg ttt gat tct aac			528
Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val Val Phe Asp Ser Asn			
140	145	150	155
acc aac agg ata gct gct cag agg cct cggt gag gag gaa cca gat tca			576
Thr Asn Arg Ile Ala Ala Gln Arg Pro Arg Glu Glu Glu Pro Asp Ser			
160	165	170	
gat tac agt gtg ata agg aag aca tag			603
Asp Tyr Ser Val Ile Arg Lys Thr			
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-5 -1 1 5 10

Thr Pro Ala Ser Ile Thr Ala Ala Lys Thr Ser Thr Ile Thr Thr Ala

15

20

25

Phe Pro Pro Val Ser Ser Thr Thr Leu Phe Ala Val Gly Ala Thr His  
30 35 40

Ser Ala Ser Ile Gln Glu Glu Thr Glu Glu Val Val Asn Ser Gln Leu  
45 50 55

Pro Leu Leu Leu Ser Leu Leu Ala Leu Leu Leu Leu Leu Val Gly  
60 65 70 75

Ala Ser Leu Leu Ala Trp Arg Met Phe Gln Lys Trp Ile Lys Ala Gly  
80 85 90

Asp His Ser Glu Leu Ser Gln Asn Pro Lys Gln Ala Ala Thr Gln Ser  
95 100 105

Glu Leu His Tyr Ala Asn Leu Glu Leu Leu Met Trp Pro Leu Gln Glu  
110 115 120

Lys Pro Ala Pro Pro Arg Glu Val Glu Val Glu Tyr Ser Thr Val Ala  
125 130 135

Ser Pro Arg Glu Glu Leu His Tyr Ala Ser Val Val Phe Asp Ser Asn  
140 145 150 155

Thr Asn Arg Ile Ala Ala Gln Arg Pro Arg Glu Glu Glu Pro Asp Ser  
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Asp Tyr Ser Val Ile Arg Lys Thr  
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<223> Description of Artificial Sequence:reverse  
translation

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<221> misc\_feature

<222> (1)..(939)

<223> n may be a, c, g, or t

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ccngtnggng gnwsnytnws ngtncartgy ccntaygara argarcaymg nacnytnaay 180

aartaytggt gymgnccncc ncarathfty ytntgygaya arathgtnga racnaarggn 240

wsngcnggna armgnaaygg nmngngtnwsn athmgngayw snccngcnaa yytnwsntty 300

c acngtnacny tngaraayyt nacngargar gaygcngna cntaytggg yggngtngay 360  
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gcnwsnacnw snatgacncc ngcnwsnath acngcngcna aracnwsnac nathacnacn 480  
gcnttyccnc cngtnwsnws nacnacnytn ttygcngtng gngcna cnca ywsngcnwsn 540  
athcargarg aracngarga rgtngttaay wsncarytnc cnytnytnyt nwsnytnytn 600  
gcnytnytny tnytnytnyt ngtnggngcn wsnytnytn cntggmgnat gttycaraar 660  
tggathaarg cngngayca ywsngarytn wsncaraayc cnaarcargc ngcnacncar 720  
wsngarytnc aytaygcnaa yytngarytn ytnatgtggc cnytncarga raarcngcn 780  
ccnccnmngng argtngargt ngartaywsn acngtngcnw snccnmngna rgarytnca 840  
taygcnwsnq tngtnnnyga ywsnaayacn aaymgnathg cngcncarmg nccnmngar 900  
gargarccng aywsngayta ywsngtnath mgnaaracn 939

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<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:reverse  
translation

<220>

<221> misc\_feature

<222> (1)..(600)

<223> n may be a, c, g, or t

<400> 9

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aaracnwsna cnathacnac ngcnttyccn ccngtnwsnw snacnacnyt nttygcngtn 180  
ggngcna cncnacnc aywsngcnws nathcargar garacngarg argtngtnaa ywsncarytn 240  
ccnytnytny tnwsnytnyt ngcnytnytn ytnytnytny tngtnggngc nwsnytnytn 300  
gcntggmgnat tgtycaraa rtggathaarg cngngayc aywsngaryt nwsncaraay 360  
ccnaarcarg cngcna cnca rwsngarytn caytaygcna ayytngaryt nytnatgtgg 420  
ccnytncarg araarcngc nccnccnmgn gargtngarg tngartayws nacngtngcn 480  
wsnccnmngng argarytnca ytaygcnwsn gtngtnnnyg aywsnaayac naaymgnath 540

gcnngcncarm gnccnmgnrgargarccn gaywsngayt aywsngtnat hmgnaaracn 600